Amendments to the Specification:

Please replace the Sequence Listing with the substitute Sequence Listing filed herewith.

Please replace the title with the following amended title:

NUCLEIC ACIDS ENCODING OPIATE RECEPTORS

Please replace the paragraph starting on page 2, line 19 with the following amended paragraph:

The present invention is based on the discovery of nucleic acid that encodes a polypeptide having mu3 opiate receptor activity. The term "mu3 opiate receptor" as used herein refers to a cell surface polypeptide that has a higher affinity for morphine than that for the opioid polypeptide [Tyr-D-Ala^2, Gly-N-Me-Phe^4, Gly(ol)^5]-enkephalin (DAMGO; SEQ ID NO:29). The interaction of morphine with a mu3 opiate receptor can induce changes in intracellular calcium concentration and nitric oxide release. Isolated nucleic acid molecules that encode a polypeptide having mu3 opiate receptor activity, host cells containing such isolated nucleic acid molecules, and substantially pure polypeptides having mu3 opiate receptor activity are particularly useful to research scientists since these materials allow scientists to explore, for example, the interactions of morphine with the mu3 opiate receptor, the molecular mechanisms by which morphine induces intracellular calcium concentration changes, and the relationships of mu3 opiate receptors with other mu opioid receptors. In addition, the methods and materials described herein can be used to provide cells that are responsive to morphine. For example, cells can be transfected with a vector that directs expression of a polypeptide having mu3 opiate receptor activity such that those cells can respond to morphine stimulation.

Please replace the paragraph starting on page 9, line 7 with the following amended paragraph:

A length and percent identity over that length for any nucleic acid or amino acid sequence is determined as follows. First, a nucleic acid or amino acid sequence is compared to

the identified nucleic acid or amino acid sequence using the BLAST 2 Sequences (Bl2seq) program from the stand-alone version of BLASTZ containing BLASTN version 2.0.14 and BLASTP version 2.0.14. This stand-alone version of BLASTZ can be obtained from the State University of New York – Old Westbury campus library as well as at Fish & Richardson's web site (~~www.fr.com~~ "www" dot "fr" dot "com") or the U.S. government's National Center for Biotechnology Information web site (~~www.ncbi.nlm.nih.gov~~ "www" dot "ncbi" dot "nlm" dot "nih" dot "gov"). Instructions explaining how to use the Bl2seq program can be found in the readme file accompanying BLASTZ. Bl2seq performs a comparison between two sequences using either the BLASTN or BLASTP algorithm. BLASTN is used to compare nucleic acid sequences, while BLASTP is used to compare amino acid sequences. To compare two nucleic acid sequences, the options are set as follows: -i is set to a file containing the first nucleic acid sequence to be compared (e.g., C:\seq1.txt); -j is set to a file containing the second nucleic acid sequence to be compared (e.g., C:\seq2.txt); -p is set to blastn; -o is set to any desired file name (e.g., C:\output.txt); -q is set to –1; -r is set to 2; and all other options are left at their default setting. For example, the following command can be used to generate an output file containing a comparison between two sequences: C:\Bl2seq –i c:\seq1.txt –j c:\seq2.txt –p blastn –o c:\output.txt –q –1 –r 2. To compare two amino acid sequences, the options of Bl2seq are set as follows: -i is set to a file containing the first amino acid sequence to be compared (e.g., C:\seq1.txt); -j is set to a file containing the second amino acid sequence to be compared (e.g., C:\seq2.txt); -p is set to blastp; -o is set to any desired file name (e.g., C:\output.txt); and all other options are left at their default setting. For example, the following command can be used to generate an output file containing a comparison between two amino acid sequences: C:\Bl2seq –i c:\seq1.txt –j c:\seq2.txt –p blastp –o c:\output.txt. If the target sequence shares homology with any portion of the identified sequence, then the designated output file will present those regions of homology as aligned sequences. If the target sequence does not share homology with any portion of the identified sequence, then the designated output file will not present aligned sequences. Once aligned, a length is determined by counting the number of consecutive nucleotides or amino acid residues from the target sequence presented in alignment with

sequence from the identified sequence starting with any matched position and ending with any other matched position. A matched position is any position where an identical nucleotide or amino acid residue is presented in both the target and identified sequence. Gaps presented in the target sequence are not counted since gaps are not nucleotides or amino acid residues. Likewise, gaps presented in the identified sequence are not counted since target sequence nucleotides or amino acid residues are counted, not nucleotides or amino acid residues from the identified sequence.